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RAW SEQUENCE LISTING

DATE: 11/19/2001

PATENT APPLICATION: US/09/935,390A

TIME: 15:40:33

Input Set : N:\Crf3\RULE60\09935390A.txt

Output Set: N:\CRF3\11192001\I935390A.raw

SEQUENCE LISTING

C--> 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Escobedo, Jaime

6 Quianjin, Hu

7 Garcia, Pablo

8 Williams, Lewis T.

9 Kothakota, Srinivas

C--> 11 (ii) TITLE OF INVENTION: Secreted Human Proteins

13 (iii) NUMBER OF SEQUENCES: 38

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Chiron Corporation

17 (B) STREET: 4560 Horton Street

18 (C) CITY: Emeryville

19 (D) STATE: CA

20 (E) COUNTRY: USA

21 (F) ZIP: 94608-2916

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Diskette

25 (B) COMPUTER: IBM Compatible

26 (C) OPERATING SYSTEM: DOS

27 (D) SOFTWARE: FastSEQ for Windows Version 2.0

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/935,390A

C--> 31 (B) FILING DATE: 22-Aug-2001

32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 08/988,671

36 (B) FILING DATE: 1997-12-11

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Jane E. R. Potter

40 (B) REGISTRATION NUMBER: 33,332

41 (C) REFERENCE/DOCKET NUMBER: 1369.002

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (510) 923-2718

45 (B) TELEFAX: (510) 655-3542

46 (C) TELEX:

49 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 2063 base pairs

52 (B) TYPE: nucleic acid

53 (C) STRANDEDNESS: single

54 (D) TOPOLOGY: linear

55 (ix) FEATURE:

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

58 GAATTCGGCA CGAGGCCTCA GTCTTCCAGG GCGGCGGTGG GTGTCCGCTT CTCTCTGCTC 60

59 TTCGACTGCA CCGCACTCGC GCGTGACCCT GACTCCCCCT AGTCAGCTCA GCGGTGCTGC 120

60 CATGGCGTGG CGGCGGCGCG AAGCCGGCGT CGGGGCTCGC GCGGTGTTGG CTCTGGCGTT 180

ENTERED

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61 GCTCGCCCTG GCCCTGTGCG TGCCCCGGGGC CCGGGGGCCGG GCTCTCGAGT GGTTCCTCGGC 240
62 CGTGGTAAAC ATCGAGTACG TGGACCCGCA GACCAACCTG ACGGTGTGGA GCGTCTCGGA 300
63 GAGTGGCCGC TTCGGCGACA GCTCGCCCAA GGAGGGCGCG CATGGCCTGG TGGGCGTCCC 360
64 GTGGGCGCCC GGCGGAGACC TCGAGGGCTG CGCGCCCGAC ACGCGCTTCT TCGTGCCCGA 420
65 GCGCGGCGGC CGAGGGGCGG CGCCCTGGGT CGCCCTGGTG GCTCGTGGGG GCTGCACCTT 480
66 CAAGGACAAG GTGCTGGTGG CGGCGCGGAG GAACGCCTCG GCCGTCTGCC TCTACAATGA 540
67 GGAGCGCTAC GGAACATCA CTTGCCCCAT GTCTCACGCG GGAACAGGAA ATATAGTGGT 600
68 CATTATGATT AGCTATCCAA AAGGAAGAGA AATTTTGGAG CTGGTGCAAA AAGGAATTCC 660
69 AGTAACGATG ACCATAGGGG TTGGCACCCG GCATGTACAG GAGTTCATCA GCGGTCAGTC 720
70 TGTGGTGTTT GTGGCCATTG CCTTCATCAC CATGATGATT ATCTCGTTAG CCTGGCTAAT 780
71 ATTTTACTAT ATACAGCGTT TCCTATATAC TGGCTCTCAG ATTGGAAGTC AGAGCCATAG 840
72 AAAAGAACT AAGAAAGTTA TTGGCCAGCT TCTACTTCAT ACTGTAAAGC ATGGAGAAAA 900
73 GGGAATTGAT GTTGATGCTG AAAATTGTGC AGTGTGTATT GAAAATTTCA AAGTAAAGGA 960
74 TATTATTAGA ATTCTGCCAT GCAAGCATAT TTTTCATAGA ATATGCATTG ACCCATGGCT 1020
75 TTTGGATCAC CGAACATGTC CAATGTGTAA ACTTGATGTC ATCAAAGCCC TAGGATATTG 1080
76 GGGAGAGCCT GGGGATGTAC AGGAGATGCC TGCTCCAGAA TCTCCTCCTG GAAGGGATCC 1140
77 AGCTGCAAT TTGAGTCTAG CTTTACCAGA TGATGACGGA AGTGATGACA GCAGTCCACC 1200
78 ATCAGCCTCC CCTGCTGAAT CTGAGCCACA GTGTGATCCC AGCTTTAAAG GAGATGCAGG 1260
79 AGAAAATACG GCATTGCTAG AAGCCGGCAG GAGTGACTCT CGGCATGGAG GACCCATCTC 1320
80 CTAGCACACG TGCCCACTGA AGTGGCACCACACAGAAGTTT GGCTTGAACT AAAGGACATT 1380
81 TTATTTTTTT TACTTTAGCA CATAATTTGT ATATTTGAAA ATAATGTATA TTATTTTACC 1440
82 TATTAGATTC TGATTGATA TACAAAGGAC TAAGATATTT TCTTCTTGAA GAGACTTTTC 1500
83 GATTAGTCCT CATATATTTA TCTACTAAAA TAGAGTGTTT ACCATGAACA GTGTGTTGCT 1560
84 TCAGACTATT ACAAGACAA CTGGGGCAGG TACTCTAATA TAAAGGACAG GTGGTGTTC 1620
85 TAAATAATTG GCTGCTATGG TTCTGTAAACCAGTTAAT TCTATTTTTC AAGGTTTTTC 1680
86 GCAAAGCACA TCAATGTTAG ACTAGTTGAA GTGGAATTGT ATAATTCAAT TCGATAATTG 1740
87 ATCTCATGGG CTTTCCCTGG AGGAAAGGTT TTTTTTGTG TTTTTTTTTT AAGAAGTTGA 1800
88 AACTTGTAAG CTGAGATGTC TGAGCTTTT TTGCCCATCT GTAGTGATG TGAAGATTTT 1860
89 AAAACCTGAG AGCACTTTTT CTTTGTTTAG AATTATGAGA AAGGCACTAG ATGACTTTAG 1920
90 GATTTGCATT TTTCCCTTTA TTGCCTCATT TCTGTGACG CCTTGTGGG GAGGGAAATC 1980
91 TGTTTATTTT TTCCTACAAA TAAAAAGCTA AGATTCTATA TCGCAAAAAA AAAAAAAAAA 2040
92 AAAAAAAAAA TTCCTGCGGC CGC 2063
94 (2) INFORMATION FOR SEQ ID NO: 2:
95 (i) SEQUENCE CHARACTERISTICS:
96 (A) LENGTH: 1328 base pairs
97 (B) TYPE: nucleic acid
98 (C) STRANDEDNESS: single
99 (D) TOPOLOGY: linear
100 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
102 GAATTTCGCA CGAGGTAGGC AAGGGATAAA AAGGCACCTA AGGCCCTTTT GCAATAAGAA 60
103 GCCAGATGGA TAAAGGAAGT GCTGGTCACC CTGGAGGTGT ACTGGTTTGG GGAAGGTCCC 120
104 CGGCCCCCAC AGCCCTCTGG GGAGCCTCAC CCTGGCTCTC CCCACTCAC TCAGCCCTCA 180
105 GGCAGCCCCT CCACAGGGCC CCTCTCCTGC CTGGACAGCT CTGCTGGTCT CCCCCTCCCC 240
106 TGGAGAAGAA CAAGGCCATG GGTGCGCCCC TGCTGCTGCC CCTGCTGCTC CTGCTGCAGC 300
107 CGCCAGCATT TCTGCAGCCT GGTGGCTCCA CAGGATCTGG TCCAAGCTAC CTTTATGGGG 360
108 TCACTCAACC AAAACACCTC TCAGCCTCCA TGGGTGGCTC TGTGGAAATC CCCTTCTCCT 420
109 TCTATTACCC CTGGGAGTTA GCCATAGTTC CCAACGTGAG AATATCCTGG AGACGGGGCC 480
110 ACTTCCACGG GCAGTCCTTC TACAGCACA GCGCCCTTC CATTCAAG GATTATGTGA 540
111 ACCGGCTCTT TCTGAAGTGG ACAGAGGGTC AGGAGAGCGG CTTCTCAGG ATCTCAAACC 600

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112 TGC GGAAGGA GGACCA GTCT GTGTATTTCT GCCGAGTCGA GCTGGACACC CGGAGATCAG 660
113 GGAGGCAGCA GTTGCA GTCC ATCAAGGGGA CCAAATCAC CATCACCCAG GCTGTCACAA 720
114 CCACCACCAC CTGGAGGCCC AGCAGCACAA CCACCATAGC CGGCCTCAGG GTCACAGAAA 780
115 GCAAAGGGCA CTCAGAATCA TGGCACCTAA GTCTGGACAC TGCCATCAGG GTTGCAATTGG 840
116 CTGTCGCTGT GCTCAAAACT GTCATTTTGG GACTGCTGTG CCTCCTCCTC CTGTGGTGGA 900
117 GGAGAAGGAA AGGTAGCAGG GCGCCAAGCA GTGACTTCTG ACCAACAGAG TGTGGGGAGA 960
118 AGGGATGTGT ATTAGCCCCG GAGGACGTGA TGTGAGACCC GCTTGTGAGT CCTCCACACT 1020
119 CGTTCCCAT TGGCAAGATA CATGGAGAGC ACCCTGAGGA CCTTTAAAAG GCAAAGCCGC 1080
120 AAGGCAGAAG GAGGCTGGGT CCCTGAATCA CCGACTGGAG GAGAGTTACC TACAAGAGCC 1140
121 TTCATCCAGG AGCATCCACA CTGCAATGAT ATAGGAATGA GGTCTGAACT CCACTGAATT 1200
122 AAACCACTGG CATTTGGGGG CTGTTTATTA TAGCAGTGCA AAGAGTTCCT TTATCCTCCC 1260
123 CAAGGATGGA AAAATACAAT TTATTTTGCT TACCATAAAA AAAAAAAAAA AAAAATTCCT 1320
124 GCGGCCGC 1328
126 (2) INFORMATION FOR SEQ ID NO: 3:
127 (i) SEQUENCE CHARACTERISTICS:
128 (A) LENGTH: 1689 base pairs
129 (B) TYPE: nucleic acid
130 (C) STRANDEDNESS: single
131 (D) TOPOLOGY: linear
132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
134 GAATTCGGCA CGAGGGCAAG ATTCGATACA AAACCAATGA ACCTGTGTGG GAGGAAAAC 60
135 TCACCTTTCTT CATTCACAAAT CCCAAGCGCC AGGACCTTGA AGTTGAGGTC AGAGACGAGC 120
136 ACACCAAGTG TTCCCTGGGG AACCTGAAGG TCCCCCTCAG CCAGCTGCTC ACCAGTGAGG 180
137 ACATGACTGT GAGCCAGCGC TTCCAGCTCA GTAACCTCGG TCCAAACAGC ACCATCAAGA 240
138 TGAAGATTGC CCTGCGGGTG CTCCATCTCG AAAAGCGAGA AAGGCCTCCA GACCACCAAC 300
139 ACTCAGCTCA AGTCAAACGT CCCTCTGTGT CCAAAGAGGG GAGGAAAACA TCCATCAAAT 360
140 CTCATATGTC TGGGTCTCCA GGCCCTGGTG GCAGCAACAC AGCTCCATCC ACACCACTCA 420
141 TTGGGGGCGAG TGATAAGCCT GGTATGGAAG AAAAGGCCCA GCCCCCTGAG GCCGGCCCTC 480
142 AGGGGCTGCA CGACCTGGGC AGAAGCTCCT CCAGCCTCCT GGCCTCCCCA GGCCACATCT 540
143 CAGTCAAGGA GCCGACCCCC AGCATCGCCT CGGACATCTC GCTGCCCATC GCCACCCAGG 600
144 AGCTGCGGCA AAGGCTGAGG CAGCTGGAAC ACGGGACGAC CCTGGGACAG TCTCCACTGG 660
145 GGCAGATCCA GCTGACCATC CGGCACAGCT CGCAGAGAAA CAAGCTTATC GTGGTCGTGC 720
146 ATGCCTGCAG AAACCTCATT GCCTTCTCTG AAGACGGCTC TGACCCCTAT GTCCGCATGT 780
147 ATTTATTACC AGACAAGAGG CGGTCAGGAA GGAGGAAAAC ACACGTGTCA AAGAAAACAT 840
148 TAAATCCAGT GTTTGATCAA AGCTTTGATT TCAGTGTTTC GTTACCAGAA GTGCAGAGGA 900
149 GAACGCTCGA CGTTGCCGTG AAGAACAGTG GCGGCTTCCT GTCCAAAGAC AAAGGGCTCC 960
150 TTGGCAAAGT ATTGGTTGCT CTGGCATCTG AAGAACTTGC CAAAGGCTGG ACCCAGTGGT 1020
151 ATGACCTCAC GGAAGATGGG ACGAGGCCTC AGGCGATGAC ATAGCCGCAG CAGGCAGGAG 1080
152 CGCTCCTCTT CAGCGTAGCT CTCCACCTCT ACCCGGAACA CACCCTCTCA CAGACGTACC 1140
153 AATGTTATTT TTATAATTTT ATGGATTTAG TTATACATAC CTTAATAGTT TTATAAAATT 1200
154 GTTGACATTT CAGGCAAATT TGGCCAATAT TATCATTGAA TTTTCTGTGT TGGATTTCTT 1260
155 CTAGGATTTT GCCAGTTCTT ACAACGTGCA GTAGGGCGGC GGTAGCTCTT GTGTCTGTGG 1320
156 ACTCTGCTCA GCTGTGTCCG TAGGAGTCGG ATGTGTCTGT GCTTTATTAT GGCTTGTGTT 1380
157 ATATATCACT GAGGTATACT ATGCCATGTA AATAGACTAT TTTTATAAAT CTTAACATGC 1440
158 TGGTTTAAAT TCAGAAGGAA ATAGATCAAG GAAATATATA TATTTTCTTC TAAACCTTAT 1500
159 TAAATTCGTG TGACAAATAA TCATTTTCAT CTTGGCAGCA AAAAGTTCTC AGTGACCTAT 1560
160 TTTGTGGTGT TTCTTTTGA AAAGAAAAGC TGAAATATTA TTAAATGCTA GTATGTTTCT 1620
161 GCCCATTATG AAAGATGAAA TAAAGTATTC AAAATATTAA AAAAAAAAAA AAAAATTCCT 1680
162 TGCGGCCGC 1689

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Output Set: N:\CRF3\11192001\I935390A.raw

165 (2) INFORMATION FOR SEQ ID NO: 4:

166 (i) SEQUENCE CHARACTERISTICS:

167 (A) LENGTH: 1505 base pairs

168 (B) TYPE: nucleic acid

169 (C) STRANDEDNESS: single

170 (D) TOPOLOGY: linear

171 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

173	GAATTCGGCA	CGAGGAGCAG	ATCTGCAAGA	GTTTCGTTTA	TGGAGGCTGC	TTGGGCAACA	60
174	AGAACAAC	CTTCGGGAA	GAAGAGTGCA	TTCTAGCCTG	TCGGGGTGTG	CAAGGTGGGC	120
175	CTTTGAGAGG	CAGCTCTGGG	GCTCAGGCGA	CTTTCCCCCA	GGGCCCCTCC	ATGGAAAGGC	180
176	GCCATCCAGT	GTGCTCTGGC	ACCTGTCAGC	CCACCCAGTT	CCGCTGCAGC	AATGGCTGCT	240
177	GCATCGACAG	TTTCCTGGAG	TGTGACGACA	CCCCAACTG	CCCCGACGCC	TCCGACGAGG	300
178	CTGCCTGTGA	AAAATACACG	AGTGGCTTTG	ACGAGCTCCA	CGCATCCAT	TTCCCCAGCG	360
179	ACAAAGGGCA	CTGCGTGGAC	CTGCCAGACA	CAGGACTCTG	CAAGGAGAGC	ATCCCGCGCT	420
180	GGTACTACAA	CCCCTTCAGC	GAACACTGCG	CCCGCTTTAC	CTATGGTGGT	TGTTACGGCA	480
181	ACAAGAACAA	CTTTGAGGAA	GAGCAGCAGT	GCCTCGAGTC	TTGTGCGGGC	ATCTCCAAGA	540
182	AGGATGTGTT	TGGCCTGAGG	CGGGAAATCC	CCATTCCCAG	CACAGGCTCT	GTGGAGATGG	600
183	CTGTCGCAGT	GTTCTGGTTC	ATCTGCATTG	TGGTGGTGGT	AGCCATCTTG	GGTACTGCT	660
184	TCTTCAAGAA	CCAGAGAAAG	GACTTCCACG	GACACCACCA	CCACCCACCA	CCCACCCCTG	720
185	CCAGCTCCAC	TGTCTCCACT	ACCGAGGACA	CGGAGCACCT	GGTCTATAAC	CACACCACGC	780
186	GGCCCCCTCTG	AGCCTGGGTC	TCACCGGCTC	TCACCTGGCC	CTGCTTCCTG	CTTGCCAAGG	840
187	CAGAGGCCTG	GGCTGGGAAA	AACTTTGGAA	CCAGACTCTT	GCCTGTTTCC	CAGGCCCACT	900
188	GTGCCTCAGA	GACCAGGGCT	CCAGCCCCTC	TTGGAGAAGT	CTCAGCTAAG	CTCACGTCCT	960
189	GAGAAAGCTC	AAAGGTTTGG	AAGGAGCAGA	AAACCTTGG	GCCAGAAGTA	CCAGACTAGA	1020
190	TGGACCTGCC	TGCATAGGAG	TTTGGAGGAA	TTTGAGTTT	TGTTTCCTCT	GTTCAAAGCT	1080
191	GCCTGTCCCT	ACCCCATGGT	GCTAGGAAGA	GGAGTGGGGT	GGTGTACAGC	CCTGGAGGCC	1140
192	CCAACCCTGT	CCTCCCGAGC	TCCTCTTCCA	TGCTGTGCGC	CCAGGGCTGG	GAGGAAGGAC	1200
193	TTCCCTGTGT	AGTTTGTGCT	GTAAAGAGTT	GCTTTTGTG	TATTTAATGC	TGTGGCATGG	1260
194	GTGAAGAGGA	GGGGAAGAGG	CCTGTTTGGC	CTCTCTATCC	TCTCTTCCTC	TTCCCCCAAG	1320
195	ATTGAGCTCT	CTGCCCTTGA	TCAGCCCCAC	CCTGGCCTAG	ACCAGCAGAC	AGAGCCAGGA	1380
196	GAAGCTCAGC	TGCATTCCGC	AGCCCCCACC	CCCAAGGTTT	TCCAACATCA	CAGCCCAGCC	1440
197	CGCCCACTGG	GTAATAAAAG	TGGTTTGTGG	AAAAAAAAAA	AAAAAAAAAA	AAGTCCTGCG	1500
198	GCCGC						1505

200 (2) INFORMATION FOR SEQ ID NO: 5:

201 (i) SEQUENCE CHARACTERISTICS:

202 (A) LENGTH: 2002 base pairs

203 (B) TYPE: nucleic acid

204 (C) STRANDEDNESS: single

205 (D) TOPOLOGY: linear

206 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

208	GAATTCGGCA	CGAGGGCCAT	GGCCGGGCTA	TCCCGCGGGT	CCGCGCGCGC	ACTGCTCGCC	60
209	GCCCTGCTGG	CGTCGACGCT	GTTGGCGCTG	CTCGTGTGCG	CCGCGCGGGG	TCGCGGCGGC	120
210	CGGGACCACG	GGGACTGGGA	CGAGGCCTCC	CGGCTGCCGC	CGCTACCACC	CCGCGAGGAC	180
211	GCGGCGCGCG	TGGCCCGCTT	CGTGACGCAC	GTCTCCGACT	GGGGCGCTCT	GGCCACCATC	240
212	TCCACGCTGG	AGGCGGTGCG	CGGCCGGCCC	TTCCGCCGAC	TCCTCTCGCT	CAGCGACGGG	300
213	CCCCGGGGCG	CGGGCAGCGG	CGTGCCCTAT	TTCTACCTGA	GCCCGCTGCA	GCTCTCCGTG	360
214	AGCAACCTGC	AGGAGAATCC	ATATGCTACA	CTGACCATGA	CTTTGGCACA	GACCAACTTC	420
215	TGCAAGAAAC	ATGGATTTGA	TCCACAAAGT	CCCTTTGTG	TTACATAAT	GCTGTCAGGA	480
216	ACTGTGACCA	AGGTGAATGA	AACAGAAATG	GATATTGCAA	AGCATTTCGT	ATTCATTCCA	540

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217 CACCCTGAGA TGAAACCTG GCCTTCCAGC CATAATTGGT TCTTTGCTAA GTTGAATATA 600
218 ACCAATATCT GGGTCCTGGA CTACTTTGGT GGACCAAAAA TCGTGACACC AGAAGAATAT 660
219 TATAATGTCA CAGTTCAGTG AAGCAGACTG TGGTGAATTT AGCAACACTT ATGAAGTTTC 720
220 TTAAAGTGGC TCATACACAC TTAAAAGGCT TAATGTTTCT CTGGAAAGCG TCCCAGAATA 780
221 TTAGCCAGTT TTCTGTCACA TGCTGGTTTG TTTGCTTGCT TGTTTACTTG CTTGTTTACC 840
222 AATAGAGTTG ACCTGTTATT GGATTTCTCT GAAGATGTGG TAGCTACTTT TTTCTATTAT 900
223 TGAAGCCATT TTCGTAGAGA AATATCCTTC ACTATAATCA AATAAGTTTT GTCCCATCAA 960
224 TTCCAAAGAT GTTTCAGTG GTGCTCTTGA AGAGGAATGA GTACCAGTTT TAAATTGCCC 1020
225 ATTGGCATTG GAAGGTAGTT GAGTATGTGT TCTTTATTCC TAGAAGCCAC TGTGCTTGGT 1080
226 AGAGTGCATC ACTCACCACA GCTGCCTCTT GAGCTGCCTG AGCCTGGTGC AAAAGGATTG 1140
227 GCCCCCATTA TGGTGCTTCT GAATAAATCT TGCCAAGATA GACAAACAAT GATGAAACTC 1200
228 AGATGGAGCT TCCTACTCAT GTTGATTTAT GTCTCACAAT CCTGGGTATT GTTAATTCAA 1260
229 CATAGGGTGA AACTATTTCT GATAAAGAAC TTTTGA AAAA CTTTTTATAC TCTAAAGTGA 1320
230 TACTCAGAAC AAAAGAAAGT CATAAAACTC CTGAATTTAA TTTCCCCACC TAAGTCGAGA 1380
231 CAGTATTATC AAAACACATG TGCACACAGA TTATTTTGTG GCTCCAAAAC TGGATTGCAA 1440
232 AAGAAAGAGG AGAGATATTT TGTGTGTTCC TGGTATTCTT TTATAAGTAA AGTTACCCAG 1500
233 GCATGGACCA GCTTCAGCCA GGGACAAAAT CCCCTCCCAA ACCACTCTCC ACAGCTTTTT 1560
234 AAAAACTATT CTACTCTTAA CAATTACCTA AGGTTCTTTC AAACCCCCC AACTCTTAAT 1620
235 AGCTTCTAGT GCTGCTACAA TCTAAGTCAG GTCACCAGAG GGAAGAGAAC ATGGCATTAA 1680
236 AAGAATCACA TCTTCAGAAG AGAAGACACT AATATTATTA CCCATATACA TGATTTTCAA 1740
237 AGATGACATA AGATTCTCTT TAAAGAGGAA ATGTCAGGAA TCAAGCCACT GAATCCTTAA 1800
238 AGAGAAAAGT TGAATATGAG TCATTGTGTC TGAAAACGTC AAAGTGAAC TAAGTGAGAT 1860
239 CCAGCAAACA GGTTCGTGTT AAGAAAAATA ATTTATACTA AATTTAGTAA AATGGACTTC 1920
240 TTATTCAAAG CATCAATAAT TAAAAGAATT ATTTTAAAAA AAAAAAAAAA AAAAAAAAAA 1980
241 AAAAAAAAAA TCCTGCGGCC GC
242
243 (2) INFORMATION FOR SEQ ID NO: 6:
244 (i) SEQUENCE CHARACTERISTICS:
245 (A) LENGTH: 1322 base pairs
246 (B) TYPE: nucleic acid
247 (C) STRANDEDNESS: single
248 (D) TOPOLOGY: linear
249 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
251 GAATTCGGCA CGAGGGCCAC GACTCTGCTG GCATTTCTTC TATAGCCACT GGAATCTGAT 60
252 CTGATTGTC TTCCACTACT ACCAGGCCAT CACCACTCCG CCTGGGTACC CACCCAGGG 120
253 CAGGAATGAT ATCGCCACCG TCTCCATCTG TAAGAAGTGC ATTTACCCCA AGCCAGCCCG 180
254 AACACACCAC TGCAGCATCT GCAACAGGTG TGTGCTGAAG ATGGATCACC ACTGCCCTG 240
255 GCTAAACAAT TGTGTGGGCC ACTATAACCA TCGGTACTTC TTCTCTTTCT GCTTTTTTCT 300
256 GACTCTGGGC TGTGTCTACT GCAGCTATGG AAGTTGGGAC CTTTCCGGG AGGCTTATGC 360
257 TGCCATTGAG AAAATGAAAC AGCTCGACAA GAACAACTA CAGGCGGTG CCAACCAGAC 420
258 TTATCACCAG ACCCCACCAC CCACCTTCTC CTTTCGAGAA AGGATGACTC ACAAGAGTCT 480
259 TGTCTACCTC TGGTTCCTGT GCAGTTCTGT GGCACTTGCC CTGGGTGCCC TAACTGTATG 540
260 GCATGCTGTT CTCATCAGTC GAGGTGAGAC TAGCATCGAA AGGCACATCA ACAAGAAGGA 600
261 GAGACGTCGG CTACAGGCCA AGGGCAGAGT ATTTAGGAAT CCTTACAAC ACGGCTGCTT 660
262 GGACAACTGG AAGGTATTCC TGGGTGTGGA TACAGGAAGG CACTGGCTTA CTCGGGTGCT 720
263 CTTACCTTCT CTTACTTTCG CCGATGGGAA TGGATGAGC TGGGAGCCCC CTCCTGGGT 780
264 GACTGCTCAC TCAGCCTCTG TGATGGCAGT GTGAGCTGGA CTGTGTCAGC CACGATCGA 840
265 GCACTCATTC TGCTCCCTAT GTTATTTCAA GGGCCTCCAA GGGCAGCTTT TCTCAGAATC 900
266 CTTGATCAAA AAGAGCCAGT GGGCCTGCCT TAGGGTACCA TGCAGGACAA TTCAAGGACC 960
267 AGCCTTTTAA CCACTGCAGA AGAAAGACAC AATGTGGAGA AATCTTAGGA CTGACATCCC 1020

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VERIFICATION SUMMARY

DATE: 11/19/2001

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TIME: 15:40:34

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Output Set: N:\CRF3\11192001\I935390A.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:11 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:56 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1
L:714 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20
L:798 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21
L:864 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22
L:931 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23
L:980 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:1032 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:1081 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
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L:1289 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:1350 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:1408 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:1490 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:1548 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33
L:1630 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
L:1704 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35
L:1768 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36
L:1820 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=37
L:1920 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=38